

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Continuation Application:

BROWN, *et al.*

Art Unit: To Be Assigned

Appln. No.: To Be Assigned

Examiner: To Be Assigned

Filed: Herewith

Atty. Docket: 16517.257

For: Nucleic Acid Molecules and Other
Molecules Associated with the
Gibberellin Pathway

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, DC 20231

Sir:

Prior to examination on the merits, Applicants hereby request entry of the following
amendments in the above-captioned application:

AMENDMENT

In the Specification:

Please amend the specification as follows:

In the specification, please replace the paragraph on page 1, beginning at line 3, and
ending at line 19 with the following paragraphs:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation application of and claims priority under 35 U.S.C §120
to Application No. 09/252,974 filed February 19, 1999 which claims priority under 35 U.S.C. §
119(e) and/or 35 U.S.C. § 120 of applications No. 60/074,201 filed February 10, 1998, No.
60/075460 filed February 19, 1998, No. 60/075463 filed February 19, 1998, No. 60/076,709 filed
March 4, 1998, No. 60/077231 filed March 9, 1998, No. 60/077230 filed March 9, 1998, No.

60/078368 filed March 18, 1998, No. 60/080844 filed April 7, 1998, No. 60/083067 filed April 27, 1998, No. 60/083387 filed April 29, 1998, No. 60/083388 filed April 29, 1998, No. 60/083389 filed April 29, 1998, No. 60/084,684, filed May 8, 1998, No. 60/086186 filed May 21, 1998, No. 60/086187 filed May 21, 1998, No. 60/086185 filed May 21, 1998, No. 60/086184 filed May 21, 1998, No. 60/086183 filed May 21, 1998, No. 60/086188 filed May 21, 1998, No. 60/099667 filed September 9, 1998, No. 60/101132 filed September 21, 1998, No. 60/101344 filed September 22, 1998, No. 60/101347 filed September 22, 1998, No. 60/104,126 filed October 13, 1998, No. 60/104,127 filed October 13, 1998, No. 60/109,018 filed November 18, 1998, No. 60/108,996 filed November 18, 1998 and No. 09/210,297 filed December 8, 1998, all of which are herein incorporated by reference in their entirety. Application No. 09/252,974 is a continuation-in part of Application No. 09/210,297, which claims priority under 35 U.S.C §119(e) and §120 to Applications 60/069,472 filed December 9, 1997, and 09/198,779 filed November 24, 1998. Application no. 09/210,297 is a continuation-in part of 09/198,779, which claims priority under 35 U.S.C §119(e) and §120 to No. 60/067,000 filed November 24, 1997, No. 60/066,873 filed November 25, 1997, No. 60/069,472 filed December 9, 1997, No. 60/074,201 filed February 10, 1998, No. 60/074,282 filed February 10, 1998, No. 60/074,280 filed February 10, 1998, No. 60/074,281 filed February 10, 1998, No. 60/074,566 filed February 12, 1998, No. 60/074,567 filed February 12, 1998, No. 60/074,565 filed February 12, 1998, No. 60/075,462 filed February 19, 1998, No. 60/074,789 filed February 19, 1998, No. 60/075,459 filed February 19, 1998, No. 60/075,461 filed February 19, 1998, No. 60/075,464 filed February 19, 1998, No. 60/075,460 filed February 19, 1998, No. 60/075,463 filed February 19, 1998, No. 60/077,231 filed March 9, 1998, No. 60/077,229 filed March 9, 1998, No. 60/077,230 filed

March 9, 1998, No. 60/078,031 filed March 16, 1998, No. 60/078,368 filed March 18, 1998, No. 60/080,844 filed April 7, 1998, No. 60/083,067 filed April 27, 1998, No. 60/083,386 filed April 29, 1998, No. 60/083,387 filed April 29, 1998, No. 60/083,388 filed April 29, 1998, No. 60/083,389 filed April 29, 1998, No. 60/084,684 filed May 8, 1998, No. 60/085,245 filed May 13, 1998, No. 60/085,224 filed May 13, 1998, No. 60/085,223 filed May 13, 1998, No. 60/085,222 filed May 13, 1998, No. 60/086,186 filed May 21, 1998, No. 60/086,339 filed May 21, 1998, No. 60/086,187 filed May 21, 1998, No. 60/086,185 filed May 21, 1998, No. 60/086,184 filed May 21, 1998, No. 60/086,183 filed May 21, 1998, No. 60/086,188 filed May 21, 1998, No. 60/089,524 filed June 16, 1998, No. 60/089,810 filed June 18, 1998, No. 60/089,814 filed June 18, 1998, No. 60/091,247 filed June 30, 1998, No. 60/092,036 filed July 8, 1998, No. 60/099,667 filed September 9, 1998, No. 60/099,668 filed September 9, 1998, No. 60/099,670 filed September 9, 1998, No. 60/099,697 filed September 9, 1998, No. 60/100,674 filed September 16, 1998, No. 60/100,673 filed September 16, 1998, No. 60/100,672 filed September 16, 1998, No. 60/101,132 filed September 21, 1998, No. 60/101,130 filed September 21, 1998, No. 60/101,508 filed September 21, 1998, No. 60/101,344 filed September 22, 1998, No. 60/101,347 filed September 22, 1998, No. 60/101,343 filed September 22, 1998, No. 60/104,126 filed October 13, 1998, No. 60/104,128 filed October 13, 1998, No. 60/104,127 filed October 13, 1998, No. 60/104,124 filed October 13, 1998, No. 60/109,018 filed November 18, 1998 and 60/108,996 filed November 18, 1998.

INCORPORATION OF SEQUENCE LISTING

A paper copy of the Sequence Listing and a computer readable form of the sequence listing on diskette, containing the file named sequence.txt, which is 47,123 bytes in size (measured in MS-DOS), and which was created on September 19, 2001, are herein incorporated by reference.

In the specification, please replace the paragraph on page 10, beginning at line 10, and ending at line 18 with the following paragraph:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(www.ddbj.nig.ac.jp/); Genebank (www.ncbi.nlm.nih.gov/Web/Search/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html). Other appropriate databases include dbEST (www.ncbi.nlm.nih.gov/dbEST/index.html), SwissProt (www.ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html), PIR (www-nbrt.georgetown.edu/pir/) and The Institute for Genome Research (www.tigr.org/tdb/tdb.html).

In the specification, please replace the paragraph beginning on page 12, line 10, and ending on page 13, line 3, and replace it with the following paragraph:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol.*

Evol. 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: ([ftp.ebi.ac.uk](ftp://ftp.ebi.ac.uk)). Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms and is available by anonymous ftp at: ([ncbi.nlm.nih.gov](ftp://ncbi.nlm.nih.gov)) (directory/pub/macaw).

In the specification, please replace the paragraph on page 50, beginning at line 1, and ending at line 7, and replace it with the following paragraph:

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure to with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STSPipeline), or GeneUp (Pesole *et al.*,

BioTechniques 25:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

In the Claims:

Please amend the claims as follows:

Please cancel claims 1-7 and 9-10 and add new claims 11-20 as follows:

11. (Added) An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, and SEQ ID NO: 10.
12. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 1.
13. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 2.
14. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 3.
15. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 4.
16. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 5.

17. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 6.

18. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 7.

19. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 9.

20. (Added) The isolated nucleic acid molecule according to claim 11, wherein said isolated nucleic acid molecule comprises a nucleic acid sequence of SEQ ID NO: 10.

REMARKS

Claims 1-7 and 9-10 have been cancelled and new claims 11-20 have been added. Support for new claims 11-20 may be found throughout the specification, *e.g.*, page 39, lines 11-23 and page 40, lines 1-4 and in the original claims. No new matter enters by these amendments. The application presently contains claims 8 and 11-20.

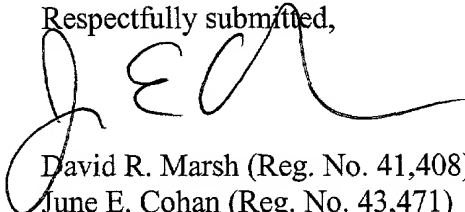
The specification has been amended to update the cross-reference to related application information and to provide the reference to the sequence listing as required by the current 37 C.F.R. §1.52. The specification has also been amended to remove “http://” and underlining on pages 10, 12, 13, and 50 of the specification. No new matter enters by these amendments.

The sequence listing has been formatted to comply with current 37 C.F.R. §1.821 et seq. and to update the prior application information. No new matter enters by this amendment

The presently pending claims are believed to be in immediate condition for allowance. Accordingly, the Examiner is respectfully requested to pass this application to issue. The Examiner is respectfully requested to contact Applicant's undersigned representative at 202.942.5071 to address any unresolved issues remaining in this application.

The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to Arnold & Porter Deposit Account No. 50-1824 referencing charge number 16517.257.

Respectfully submitted,



David R. Marsh (Reg. No. 41,408)
June E. Cohan (Reg. No. 43,471)

Date: September 19, 2001

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Marked up Specification

Page 1, lines 3 -19:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation application of and claims priority under 35 U.S.C §120 to Application No. 09/252,974 filed February 19, 1999 which claims priority under 35 U.S.C. § 119(e) and/or 35 U.S.C. § 120 of applications [No. 60/069472 filed December 9, 1997,] No. 60/074,201 filed February 10, 1998, [No. 60/074282 filed February 10, 1998, No. 60/074565 filed February 12, 1998,] No. 60/075460 filed February 19, 1998, No. 60/075463 filed February 19, 1998, No. 60/076,709 filed March 4, 1998, No. 60/077231 filed March 9, 1998, No. 60/077230 filed March 9, 1998, No. 60/078368 filed March 18, 1998, No. 60/080844 filed April 7, 1998, No. 60/083067 filed April 27, 1998, No. 60/083387 filed April 29, 1998, No. 60/083388 filed April 29, 1998, No. 60/083389 filed April 29, 1998, ["Nucleic Acid Molecules and Other Molecules Associated with the Ethylene Biosynthetic Pathway" docket No. 38-21(15097)A"] No. 60/084,684, filed May 8, 1998, No. 60/086186 filed May 21, 1998, No. 60/086187 filed May 21, 1998, No. 60/086185 filed May 21, 1998, No. 60/086184 filed May 21, 1998, No. 60/086183 filed May 21, 1998, No. 60/086188 filed May 21, 1998, No. 60/099667 filed September 9, 1998, No. 60/101132 filed September 21, 1998, No. 60/101344 filed September 22, 1998, No. 60/101347 filed September 22, 1998, No. 60/104,126 filed October 13, 1998, No. 60/104,127 filed October 13, 1998, No. 60/109,018 filed November 18, 1998, No. 60/108,996 filed November 18, 1998 and No. 09/210,297 filed December 8, 1998, all of which are herein incorporated by reference in their entirety. Application No. 09/252,974 is a continuation-in part of Application No. 09/210,297, which claims priority under 35 U.S.C §119(e) and §119(e) and

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Page 10, lines 10-18:

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(http://www.ebi.ac.uk/ebi_docs/swisprot_db/swisshome.html), PIR (<http://www-nbrt.georgetown.edu/pir/>)(*remove underlining*) and The Institute for Genome Research (<http://www.tigr.org/tdb/tdb.html>) (*remove underlining*).

Page 12, line 10-page 13, line 3:

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both pairwise alignments and multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: (<ftp.ebi.ac.uk>) (*remove underlining*). Another program is MACAW (Schuler *et al.*, *Proteins Struct. Func. Genet.* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms and is available by anonymous ftp at: (<ncbi.nlm.nih.gov>) (*remove underlining*) (directory/pub/macaw).

Page 50, line 1-7:

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure to with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) (*remove underlining*), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline) (*remove underlining*), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

TOP SECRET